<110> Walke, D. Wade
      Scoville, John

<120> Novel Human Membrane Proteins and Polynucleotides Encoding the Same

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<150> US 60/237,280
<151> 2000-10-02

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<213> homo sapiens

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caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc    420
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cctctggaca aggagctcat gacagagtcc tcactcttta accctttgtc ggacatcaaa   1320
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atcaaccaag gtgaacccag tgaaaatcca gcaaacaaag atcaaatag cttgttgaag   1680
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<210> 2
<211> 577
<212> PRT

<400> 2

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Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
          35              40              45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
      50              55              60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
 65               70              75              80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
                  85              90              95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
          100             105             110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
          115             120             125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
          130             135             140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145             150             155             160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
                  165             170             175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
          180             185             190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
          195             200             205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
      210             215             220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225             230             235             240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
              245             250             255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
          260             265             270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
          275             280             285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
          290             295             300
Leu Asp Lys Lys Pro Leu His Glu Ile Lys Pro Gln Ser Ile Glu Asn
305             310             315             320
Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala
                  325             330             335
Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser
              340             345             350
Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe
          355             360             365
Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Ala Lys Asn Ile Met Glu
      370             375             380
Leu Met Ile Gln Glu Lys Ser Phe Gly Asn Ser Leu Leu Leu Asn Ser
385             390             395             400
Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile
              405             410             415
Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu
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2

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              420             425                 430
Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met
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Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His
      450             455                 460
Ser Arg Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr Met His
465             470                 475                 480
Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr
              485                 490                 495
Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg
          500             505                 510
Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala
      515             520                 525
Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly
      530             535                 540
Glu Pro Ser Glu Asn Pro Ala Asn Lys Gly Ser Asn Ser Leu Leu Lys
545             550                 555                 560
Asn Thr Tyr Ala Ile Gly Gly Lys Ile Ser Arg His Leu Gly Ser Ser
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<210> 3
<211> 1701
<212> DNA
<213> homo sapiens

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gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc     240
atgcagatat tcttcaaatg caacggcgag tgggtccatc agaacgagca cgtctctgaa     300
gagactctgg acgagagctc aggtttgaag gtccgcgaag tgttcatcaa tgttactagg     360
caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc     420
cacctgggta cctccaagag caggaaggcc tctgtgcgca tagcctattt acggaaaaac     480
tttgaacaag acccacaagg aagggaagtt cccattgaag gcatgattgt actgcactgc     540
cgcccaccag agggagtccc tgctgccgag gtggaatggc tgaaaaatga gagcccatt      600
gactctgaac aagacgagaa cattgacacc agggctgacc ataacctgat catcaggcag     660
gcacggctct cggactcagg aaattacacc tgcatggcag ccaacatcgt ggctaagagg     720
agaagcctgt cggccactgt tgtggtctac gtggatggga gctgggaagt gtggagcgaa     780
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ggtctttgca tcctaggcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt     960
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tacagcggac ccatctgtct gcaggaccct ctggacaagg agctcatgac agagtcctca     1260
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ggagtgtctg agagagctga gtaccacggc aagaatcatt ccaggacttt ccccatgga      1380
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cgcttagtaa tgccaaatac aggggtgagc ttactcatac cacacggtgc catcccagag     1560
gagaattctt gggagattta tatgtccatc aaccaaggtg aacccagtga aaatccagca     1620
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3

<210> 4
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<212> PRT
<213> homo sapiens

<400> 4

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Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
        35              40              45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
    50              55              60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
65              70              75              80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
            85              90              95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
            100             105             110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
    115             120             125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
    130             135             140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145             150             155             160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
            165             170             175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
            180             185             190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
            195             200             205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
    210             215             220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225             230             235             240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
            245             250             255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
            260             265             270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
    275             280             285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
    290             295             300
Leu Gly Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly
305             310             315             320
Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr
            325             330             335
Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala
            340             345             350
Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Ala
            355             360             365
Lys Asn Ile Met Glu Leu Met Ile Gln Glu Lys Ser Phe Gly Asn Ser
370                 375                 380
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4

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Leu Leu Leu Asn Ser Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr
385                 390                 395                 400
Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met
                405                 410                 415
Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val
                420                 425                 430
Gln Ser Ser Phe Met Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr
                435                 440                 445
His Gly Lys Asn His Ser Arg Thr Phe Pro His Gly Asn Asn His Ser
    450                 455                 460
Phe Ser Thr Met His Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu
465                 470                 475                 480
Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly
                485                 490                 495
His Leu Gly Gly Arg Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu
                500                 505                 510
Ile Pro His Gly Ala Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met
                515                 520                 525
Ser Ile Asn Gln Gly Glu Pro Ser Glu Asn Pro Ala Asn Lys Gly Ser
    530                 535                 540
Asn Ser Leu Leu Lys Asn Thr Tyr Ala Ile Gly Gly Lys Ile Ser Arg
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His Leu Gly Ser Ser Arg
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<211> 1692
<212> DNA
<213> homo sapiens

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gcccttcccg aatccatccc atcagctcct gggacactgc ctcatttcat agaggagcca   180
gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc   240
atgcagatat tcttcaaatg caacggcgag tgggtccatc agaacgagca cgtctctgaa   300
gagactctgg acgagagctc aggtttgaag gtccgcgaag tgttcatcaa tgttactagg   360
caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc   420
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cgcccaccag agggagtccc tgctgccgag gtggaatggc tgaaaaatga gagcccatt    600
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gcacggctct cggactcagg aaattacacc tgcatggcag ccaacatcgt ggctaagagg   720
agaagcctgt cggccactgt tgtggtctac gtggatggga gctgggaagt gtggagcgaa   780
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ggtctttgca tcctagataa aaaacctctt catgaaataa aaccccaaag cattgagaat   960
gccagcgaca ttgctttgta ctcgggcttg ggtgctgccg tcgtggccgt tgcagtcctg  1020
gtcattggtg tcacccttta cagacggagc cagagtgact atggcgtgga cgtcattgac  1080
tcttctgcat tgacaggtgg cttccagacc ttcaacttca aaacagtccg tcaaggtaac  1140
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atgccaaata caggggtgag cttactcata ccacacggtg ccatcccaga ggagaattct    1560
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<211> 563
<212> PRT
<213> homo sapiens

<400> 6

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Trp Leu Pro Trp Leu Gly Leu Cys Phe Trp Ala Ala Gly Thr Ala Ala
            20                  25                  30
Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
        35                  40                  45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
    50                  55                  60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
65                  70                  75                  80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
                85                  90                  95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
            100                 105                 110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
        115                 120                 125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
    130                 135                 140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145                 150                 155                 160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
                165                 170                 175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
            180                 185                 190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
            195                 200                 205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
    210                 215                 220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225                 230                 235                 240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
                245                 250                 255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
            260                 265                 270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
        275                 280                 285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
    290                 295                 300
Leu Asp Lys Lys Pro Leu His Glu Ile Lys Pro Gln Ser Ile Glu Asn
305                 310                 315                 320
Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala
                325                 330                 335
Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser
            340                 345                 350
Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe
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6

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                 355                      360                      365
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         370                      375                      380
Asn Ser Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly
385                      390                      395                      400
Pro Ile Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser
                 405                      410                      415
Ser Leu Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser
                 420                      425                      430
Phe Met Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys
         435                      440                      445
Asn His Ser Arg Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr
         450                      455                      460
Met His Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu
465                      470                      475                      480
Pro Thr Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly
                 485                      490                      495
Gly Arg Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His
         500                      505                      510
Gly Ala Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn
         515                      520                      525
Gln Gly Glu Pro Ser Glu Asn Pro Ala Asn Lys Gly Ser Asn Ser Leu
         530                      535                      540
Leu Lys Asn Thr Tyr Ala Ile Gly Gly Lys Ile Ser Arg His Leu Gly
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Ser Ser Arg


<210> 7
<211> 1659
<212> DNA
<213> homo sapiens

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gcccttcccg aatccatccc atcagctcct gggacactgc ctcatttcat agaggagcca    180
gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc    240
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caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc    420
cacctgggta cctccaagag caggaaggcc tctgtgcgca tagcctattt acggaaaaac    480
tttgaacaag acccacaagg aagggaagtt cccattgaag gcatgattgt actgcactgc    540
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7

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aggacttttc cccatggaaa caaccacagc tttagtacaa tgcatcccag aaataaaatg  1380
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<210> 8
<211> 552
<212> PRT
<213> homo sapiens

<400> 8
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Trp Leu Pro Trp Leu Gly Leu Cys Phe Trp Ala Ala Gly Thr Ala Ala
             20                  25                  30
Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
         35                  40                  45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
     50                  55                  60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
65                  70                  75                  80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
                 85                  90                  95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
             100                 105                 110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
         115                 120                 125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
     130                 135                 140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145                 150                 155                 160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
                 165                 170                 175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
             180                 185                 190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
             195                 200                 205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
     210                 215                 220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225                 230                 235                 240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
             245                 250                 255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
             260                 265                 270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
     275                 280                 285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
     290                 295                 300
Leu Gly Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly
305                 310                 315                 320
Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr
             325                 330                 335
Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala
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8

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              340                    345                    350
Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Gly
         355                    360                    365
Asn Ser Leu Leu Leu Asn Ser Ala Met Gln Pro Asp Leu Thr Val Ser
     370                    375                    380
Arg Thr Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro Leu Asp Lys Glu
385                    390                    395                    400
Leu Met Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser Asp Ile Lys Val
                   405                    410                    415
Lys Val Gln Ser Ser Phe Met Val Ser Leu Gly Val Ser Glu Arg Ala
              420                    425                    430
Glu Tyr His Gly Lys Asn His Ser Arg Thr Phe Pro His Gly Asn Asn
         435                    440                    445
His Ser Phe Ser Thr Met His Pro Arg Asn Lys Met Pro Tyr Ile Gln
     450                    455                    460
Asn Leu Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg Thr Thr Gly Val
465                    470                    475                    480
Phe Gly His Leu Gly Gly Arg Leu Val Met Pro Asn Thr Gly Val Ser
              485                    490                    495
Leu Leu Ile Pro His Gly Ala Ile Pro Glu Glu Asn Ser Trp Glu Ile
         500                    505                    510
Tyr Met Ser Ile Asn Gln Gly Glu Pro Ser Glu Asn Pro Ala Asn Lys
         515                    520                    525
Gly Ser Asn Ser Leu Leu Lys Asn Thr Tyr Ala Ile Gly Gly Lys Ile
     530                    535                    540
Ser Arg His Leu Gly Ser Ser Arg
545                    550

<210> 9
<211> 2736
<212> DNA
<213> homo sapiens

<400> 9
atggggagag cggcggccac cgcaggcggc ggcggagggg cgcgccgctg gctcccgtgg      60
ctggggctgt gcttctgggc ggcagggacc gcggctgccc gaggaactga caatggcgaa     120
gcccttcccg aatccatccc atcagctcct gggacactgc ctcatttcat agaggagcca     180
gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc     240
atgcagatat tcttcaaatg caacggcgag tgggtccatc agaacgagca cgtctctgaa     300
gagactctgg cgagagctc aggtttgaag gtccgcgaag tgttcatcaa tgttactagg     360
caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc     420
cacctgggta cctccaagag caggaaggcc tctgtgcgca tagcctattt acggaaaaac     480
tttgaacaag acccacaagg aagggaagtt cccattgaag gcatgattgt actgcactgc     540
cgcccaccag agggagtccc tgctgccgag gtggaatggc tgaaaaatga gagcccatt      600
gactctgaac aagacgagaa cattgacacc agggctgacc ataacctgat catcaggcag     660
gcacggctct cggactcagg aaattacacc tgcatggcag ccaacatcgt ggctaagagg     720
agaagcctgt cggccactgt tgtggtctac gtggatggga ctgggaagt gtggagcgaa     780
tggtccgtct gcagtccaga gtgtgaacat ttgcggatcc gggagtgcac agcaccaccc     840
ccgagaaatg ggggcaaatt ctgtgaaggt ctaagccagg aatctgaaaa ctgcacagat     900
ggtctttgca tcctagataa aaaacctctt catgaaataa accccaaag cattgagaat     960
gccagcgaca ttgctttgta ctcgggcttg ggtgctgccg tcgtggccgt tgcagtcctg    1020
gtcattggtg tcacccttta cagacggagc cagagtgact atggcgtgga cgtcattgac    1080
tcttctgcat tgacaggtgg cttccagacc ttcaacttca aaacagtccg tcaagccaag    1140
aatatcatgg aactaatgat acaagaaaaa tcctttggta actccctgct cctgaattct    1200
gccatgcagc cagatctgac agtgagccgg acatacagcg gacccatctg tctgcaggac    1260
cctctggaca aggagctcat gacagagtcc tcactcttta acccttttgtc ggacatcaaa    1320
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9

                   —

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gtgaaagtcc agagctcgtt catggtttcc ctgggagtgt ctgagagagc tgagtaccac     1380
ggcaagaatc attccaggac tttttcccat ggaaacaacc acagctttag tacaatgcat     1440
cccagaaata aaatgcccta catccaaaat ctgtcatcac tccccacaag gacagaactg     1500
aggacaactg gtgtctttgg ccatttaggg gggcgcttag taatgccaaa tacaggggtg     1560
agcttactca taccacacgg tgccatccca gaggagaatt cttgggagat ttatatgtcc     1620
atcaaccaag gtgaacccag cctccagtca gatggctctg aggtgctcct gagtcctgaa     1680
gtcacctgtg gtcctccaga catgatcgtc accactccct ttgcattgac catcccgcac     1740
tgtgcagatg tcagttctga gcattggaat atccatttaa agaagaggac acagcagggc     1800
aaatgggagg aagtgatgtc agtggaagat gaatctacat cctgttactg ccttttggac     1860
ccctttgcgt gtcatgtgct cctggacagc tttgggacct atgcgctcac tggagagcca     1920
atcacagact gtgccgtgaa gcaactgaag gtggcggttt ttggctgcat gtcctgtaac     1980
tccctggatt acaacttgag agtttactgt gtggacaata ccccttgtgc atttcaggaa     2040
gtggtttcag atgaaaggca tcaaggtgga cagctcctgg aagaaccaaa attgctgcat     2100
ttcaaaggga atacctttag tcttcagatt tctgtccttg atattccccc attcctctgg     2160
agaattaaac cattcactgc ctgccaggaa gtcccgttct cccgcgtgtg tgtgcagtaac    2220
cggcagcccc tgcactgtgc cttctccctg gagcgttata cgcccactac cacccagctg     2280
tcctgcaaaa tctgcattcg gcagctcaaa ggccatgaac agatcctcca agtgcagaca     2340
tcaatcctag agagtgaacg agaaaccatc actttcttcg cacaagagga cagcactttc     2400
cctgcacaga ctggccccaa agccttcaaa attccctact ccatcagaca gcggatttgt     2460
gctacatttg atacccccaa tgccaaaggc aaggactggc agatgttagc acagaaaaac     2520
agcatcaaca ggaatttatc ttatttcgct acacaaagta gcccatctgc tgtcattttg     2580
aacctgtggg aagctcgtca tcagcatgat ggtgatcttg actccctggc ctgtgccctt     2640
gaagagattg ggaggacaca cacgaaactc tcaaacattt cagaatccca gcttgatgaa     2700
gccgacttca actacagcag gcaaaatgga ctctag                                2736
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<210> 10
<211> 911
<212> PRT
<213> homo sapiens

<400> 10
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Met Gly Arg Ala Ala Ala Thr Ala Gly Gly Gly Gly Ala Arg Arg
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Trp Leu Pro Trp Leu Gly Leu Cys Phe Trp Ala Ala Gly Thr Ala Ala
        20                  25                  30
Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
        35                  40                  45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
        50                  55                  60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
65                  70                  75                  80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
                85                  90                  95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
                100                 105                 110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
                115                 120                 125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
        130                 135                 140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145                 150                 155                 160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
                165                 170                 175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
                180                 185                 190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
```

10

```
              195                      200                      205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
    210                      215                      220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225                      230                      235                      240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
                245                      250                      255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
                260                      265                      270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
                275                      280                      285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
    290                      295                      300
Leu Asp Lys Lys Pro Leu His Glu Ile Lys Pro Gln Ser Ile Glu Asn
305                      310                      315                      320
Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala
                325                      330                      335
Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser
                340                      345                      350
Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe
                355                      360                      365
Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Ala Lys Asn Ile Met Glu
    370                      375                      380
Leu Met Ile Gln Glu Lys Ser Phe Gly Asn Ser Leu Leu Leu Asn Ser
385                      390                      395                      400
Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile
                405                      410                      415
Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu
                420                      425                      430
Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met
                435                      440                      445
Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His
    450                      455                      460
Ser Arg Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr Met His
465                      470                      475                      480
Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr
                485                      490                      495
Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg
                500                      505                      510
Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala
    515                      520                      525
Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly
    530                      535                      540
Glu Pro Ser Leu Gln Ser Asp Gly Ser Glu Val Leu Leu Ser Pro Glu
545                      550                      555                      560
Val Thr Cys Gly Pro Pro Asp Met Ile Val Thr Thr Pro Phe Ala Leu
                565                      570                      575
Thr Ile Pro His Cys Ala Asp Val Ser Ser Glu His Trp Asn Ile His
                580                      585                      590
Leu Lys Lys Arg Thr Gln Gln Gly Lys Trp Glu Glu Val Met Ser Val
                595                      600                      605
Glu Asp Glu Ser Thr Ser Cys Tyr Cys Leu Leu Asp Pro Phe Ala Cys
    610                      615                      620
His Val Leu Leu Asp Ser Phe Gly Thr Tyr Ala Leu Thr Gly Glu Pro
625                      630                      635                      640
Ile Thr Asp Cys Ala Val Lys Gln Leu Lys Val Ala Val Phe Gly Cys
```

11

```
                 645                  650                    655
Met Ser Cys Asn Ser Leu Asp Tyr Asn Leu Arg Val Tyr Cys Val Asp
             660                 665                 670
Asn Thr Pro Cys Ala Phe Gln Glu Val Val Ser Asp Glu Arg His Gln
         675                 680                 685
Gly Gly Gln Leu Leu Glu Glu Pro Lys Leu Leu His Phe Lys Gly Asn
     690                 695                 700
Thr Phe Ser Leu Gln Ile Ser Val Leu Asp Ile Pro Pro Phe Leu Trp
705                 710                 715                 720
Arg Ile Lys Pro Phe Thr Ala Cys Gln Glu Val Pro Phe Ser Arg Val
                 725                 730                 735
Trp Cys Ser Asn Arg Gln Pro Leu His Cys Ala Phe Ser Leu Glu Arg
             740                 745                 750
Tyr Thr Pro Thr Thr Thr Gln Leu Ser Cys Lys Ile Cys Ile Arg Gln
         755                 760                 765
Leu Lys Gly His Glu Gln Ile Leu Gln Val Gln Thr Ser Ile Leu Glu
     770                 775                 780
Ser Glu Arg Glu Thr Ile Thr Phe Phe Ala Gln Glu Asp Ser Thr Phe
785                 790                 795                 800
Pro Ala Gln Thr Gly Pro Lys Ala Phe Lys Ile Pro Tyr Ser Ile Arg
                 805                 810                 815
Gln Arg Ile Cys Ala Thr Phe Asp Thr Pro Asn Ala Lys Gly Lys Asp
             820                 825                 830
Trp Gln Met Leu Ala Gln Lys Asn Ser Ile Asn Arg Asn Leu Ser Tyr
         835                 840                 845
Phe Ala Thr Gln Ser Ser Pro Ser Ala Val Ile Leu Asn Leu Trp Glu
     850                 855                 860
Ala Arg His Gln His Asp Gly Asp Leu Asp Ser Leu Ala Cys Ala Leu
865                 870                 875                 880
Glu Glu Ile Gly Arg Thr His Thr Lys Leu Ser Asn Ile Ser Glu Ser
             885                 890                 895
Gln Leu Asp Glu Ala Asp Phe Asn Tyr Ser Arg Gln Asn Gly Leu
         900                 905                 910
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<210> 11
<211> 2703
<212> DNA
<213> homo sapiens

<400> 11
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atggggagag cggcggccac cgcaggcggc ggcggagggg cgcgccgctg gctcccgtgg    60
ctggggctgt gcttctgggc ggcagggacc gcggctgccc gaggaactga caatggcgaa   120
gcccttcccg aatccatccc atcagctcct gggacactgc ctcatttcat agaggagcca   180
gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc   240
atgcagatat tcttcaaatg caacggcgag tgggtccatc agaacgagca cgtctctgaa   300
gagactctgg acgagagctc aggtttgaag gtccgcgaag tgttcatcaa tgttactagg   360
caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc   420
cacctgggta cctccaagag caggaaggcc tctgtgcgca tagcctattt acggaaaaac   480
tttgaacaag acccacaagg aagggaagtt cccattgaag catgattgt actgcactgc    540
cgcccaccag agggagtccc tgctgccgag gtggaatggc tgaaaaatga gagcccatt    600
gactctgaac aagacgagaa cattgacacc agggctgacc ataacctgat catcaggcag   660
gcacggctct cggactcagg aaattacacc tgcatggcag ccaacatcgt ggctaagagg   720
agaagcctgt cggccactgt gtggtctac gtggatggga ctgggaagt gtggagcgaa     780
tggtccgtct gcagtccaga gtgtgaacat ttgcggatcc gggagtgcac agcaccaccc   840
ccgagaaatg ggggcaaatt ctgtgaaggt ctaagccagg aatctgaaaa ctgcacagat   900
ggtctttgca tcctaggcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt   960
```

12

```
gctgccgtcg tggccgttgc agtcctggtc attggtgtca cccctttacag acggagccag    1020
agtgactatg gcgtggacgt cattgactct tctgcattga caggtggctt ccagaccttc    1080
aacttcaaaa cagtccgtca agccaagaat atcatggaac taatgataca agaaaaatcc    1140
tttggtaact ccctgctcct gaattctgcc atgcagccag atctgacagt gagccggaca    1200
tacagcggac ccatctgtct gcaggaccct ctggacaagg agctcatgac agagtcctca    1260
ctctttaacc ctttgtcgga catcaaagtg aaagtccaga gctcgttcat ggtttccctg    1320
ggagtgtctg agagagctga gtaccacggc aagaatcatt ccaggacttt tccccatgga    1380
aacaaccaca gctttagtac aatgcatccc agaaataaaa tgccctacat ccaaaatctg    1440
tcatcactcc ccacaaggac agaactgagg acaactggtg tctttggcca tttaggggg    1500
cgcttagtaa tgccaaatac aggggtgagc ttactcatac cacacggtgc catcccagag    1560
gagaattctt gggagattta tatgtccatc aaccaaggtg aacccagcct ccagtcagat    1620
ggctctgagg tgctcctgag tcctgaagtc acctgtggtc ctccagacat gatcgtcacc    1680
actccctttg cattgaccat cccgcactgt gcagatgtca gttctgagca ttggaatatc    1740
catttaaaga gaggacaca gcagggcaaa tgggaggaag tgatgtcagt ggaagatgaa    1800
tctacatcct gttactgcct tttggacccc tttgcgtgtc atgtgctcct ggacagcttt    1860
gggacctatg cgctcactgg agagccaatc acagactgtg ccgtgaagca actgaaggtg    1920
gcggtttttg gctgcatgtc ctgtaactcc ctggattaca acttgagagt ttactgtgtg    1980
gacaataccc cttgtgcatt tcaggaagtg gtttcagatg aaaggcatca aggtggacag    2040
ctcctggaag aaccaaaatt gctgcatttc aaagggaata ccttagtct tcagatttct    2100
gtccttgata ttcccccatt cctctggaga attaaaccat tcactgcctg ccaggaagtc    2160
ccgttctccc gcgtgtggtg cagtaaccgg cagcccctgc actgtgcctt ctccctggag    2220
cgttatacgc ccactaccac ccagctgtcc tgcaaaatct gcattcggca gctcaaaggc    2280
catgaacaga tcctccaagt gcagacatca atcctagaga gtgaacgaga aaccatcact    2340
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ccctactcca tcagacagcg gatttgtgct acatttgata ccccaatgc caaaggcaag    2460
gactggcaga tgttagcaca gaaaaacagc atcaacagga atttatctta tttcgctaca    2520
caaagtagcc catctgctgt cattttgaac ctgtgggaag ctcgtcatca gcatgatggt    2580
gatcttgact ccctggcctg tgcccttgaa gagattggga ggacacacac gaaactctca    2640
aacatttcag aatcccagct tgatgaagcc gacttcaact acagcaggca aaatggactc    2700
tag                                                                   2703
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<210> 12
<211> 900
<212> PRT
<213> homo sapiens

<400> 12

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Met Gly Arg Ala Ala Ala Thr Ala Gly Gly Gly Gly Ala Arg Arg
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Trp Leu Pro Trp Leu Gly Leu Cys Phe Trp Ala Ala Gly Thr Ala Ala
             20              25              30
Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
          35              40              45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
       50              55              60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
65              70              75              80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
             85              90              95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
             100             105             110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
          115             120             125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
       130             135             140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
```

13

```
                         150                         155                            160
145
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
                     165                         170                     175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
                 180                         185                 190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
             195                     200                 205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
     210                         215                 220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225                     230                     235                     240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
                 245                     250                 255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
                 260                     265                 270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
             275                 280                 285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
         290                     295                 300
Leu Gly Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly
305                         310                 315                     320
Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr
                 325                     330                 335
Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala
             340                     345                 350
Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Ala
             355                 360                 365
Lys Asn Ile Met Glu Leu Met Ile Gln Glu Lys Ser Phe Gly Asn Ser
     370                     375                 380
Leu Leu Leu Asn Ser Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr
385                     390                 395                     400
Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met
                 405                 410                     415
Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val
             420                 425                 430
Gln Ser Ser Phe Met Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr
         435                     440                 445
His Gly Lys Asn His Ser Arg Thr Phe Pro His Gly Asn Asn His Ser
     450                     455                 460
Phe Ser Thr Met His Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu
465                     470                 475                     480
Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly
             485                 490                 495
His Leu Gly Gly Arg Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu
         500                     505                 510
Ile Pro His Gly Ala Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met
     515                     520                 525
Ser Ile Asn Gln Gly Glu Pro Ser Leu Gln Ser Asp Gly Ser Glu Val
     530                     535                 540
Leu Leu Ser Pro Glu Val Thr Cys Gly Pro Pro Asp Met Ile Val Thr
545                     550                 555                     560
Thr Pro Phe Ala Leu Thr Ile Pro His Cys Ala Asp Val Ser Ser Glu
                 565                 570                 575
His Trp Asn Ile His Leu Lys Lys Arg Thr Gln Gln Gly Lys Trp Glu
             580                 585                 590
Glu Val Met Ser Val Glu Asp Glu Ser Thr Ser Cys Tyr Cys Leu Leu
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14

```
            595                    600                    605
Asp Pro Phe Ala Cys His Val Leu Leu Asp Ser Phe Gly Thr Tyr Ala
        610                    615                    620
Leu Thr Gly Glu Pro Ile Thr Asp Cys Ala Val Lys Gln Leu Lys Val
625                    630                    635                    640
Ala Val Phe Gly Cys Met Ser Cys Asn Ser Leu Asp Tyr Asn Leu Arg
                645                    650                    655
Val Tyr Cys Val Asp Asn Thr Pro Cys Ala Phe Gln Glu Val Val Ser
                660                    665                    670
Asp Glu Arg His Gln Gly Gly Gln Leu Leu Glu Glu Pro Lys Leu Leu
            675                    680                    685
His Phe Lys Gly Asn Thr Phe Ser Leu Gln Ile Ser Val Leu Asp Ile
            690                    695                    700
Pro Pro Phe Leu Trp Arg Ile Lys Pro Phe Thr Ala Cys Gln Glu Val
705                    710                    715                    720
Pro Phe Ser Arg Val Trp Cys Ser Asn Arg Gln Pro Leu His Cys Ala
                725                    730                    735
Phe Ser Leu Glu Arg Tyr Thr Pro Thr Thr Thr Gln Leu Ser Cys Lys
                740                    745                    750
Ile Cys Ile Arg Gln Leu Lys Gly His Glu Gln Ile Leu Gln Val Gln
            755                    760                    765
Thr Ser Ile Leu Glu Ser Glu Arg Glu Thr Ile Thr Phe Phe Ala Gln
        770                    775                    780
Glu Asp Ser Thr Phe Pro Ala Gln Thr Gly Pro Lys Ala Phe Lys Ile
785                    790                    795                    800
Pro Tyr Ser Ile Arg Gln Arg Ile Cys Ala Thr Phe Asp Thr Pro Asn
                805                    810                    815
Ala Lys Gly Lys Asp Trp Gln Met Leu Ala Gln Lys Asn Ser Ile Asn
                820                    825                    830
Arg Asn Leu Ser Tyr Phe Ala Thr Gln Ser Ser Pro Ser Ala Val Ile
            835                    840                    845
Leu Asn Leu Trp Glu Ala Arg His Gln His Asp Gly Asp Leu Asp Ser
        850                    855                    860
Leu Ala Cys Ala Leu Glu Glu Ile Gly Arg Thr His Thr Lys Leu Ser
865                    870                    875                    880
Asn Ile Ser Glu Ser Gln Leu Asp Glu Ala Asp Phe Asn Tyr Ser Arg
                885                    890                    895
Gln Asn Gly Leu
            900


<210> 13
<211> 2694
<212> DNA
<213> homo sapiens


<400> 13
atggggagag cggcggccac cgcaggcggc ggcggagggg cgcgccgctg gctcccgtgg      60
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gcccttcccg aatccatccc atcagctcct gggacactgc ctcatttcat agaggagcca     180
gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc     240
atgcagatat tcttcaaatg caacggcgag tgggtccatc agaacgagca cgtctctgaa     300
gagactctgg acgagagctc aggtttgaag gtccgcgaag tgttcatcaa tgttactagg     360
caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc      420
cacctgggta cctccaagag caggaaggcc tctgtgcgca tagcctattt acggaaaaac     480
tttgaacaag acccacaagg aagggaagtt cccattgaag gcatgattgt actgcactgc     540
cgcccaccag agggagtccc tgctgccgag gtggaatggc tgaaaaatga agagcccatt     600
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15

```
gactctgaac aagacgagaa cattgacacc agggctgacc ataacctgat catcaggcag    660
gcacggctct cggactcagg aaattacacc tgcatggcag ccaacatcgt ggctaagagg    720
agaagcctgt cggccactgt tgtggtctac gtggatggga gctgggaagt gtggagcgaa    780
tggtccgtct gcagtccaga gtgtgaacat ttgcggatcc gggagtgcac agcaccaccc    840
ccgagaaatg ggggcaaatt ctgtgaaggt ctaagccagg aatctgaaaa ctgcacagat    900
ggtctttgca tcctagataa aaaacctctt catgaaataa aaccccaaag cattgagaat    960
gccagcgaca ttgctttgta ctcgggcttg ggtgctgccg tcgtggccgt tgcagtcctg   1020
gtcattggtg tcacccttta cagacggagc cagagtgact atggcgtgga cgtcattgac   1080
tcttctgcat tgacaggtgg cttccagacc ttcaacttca aaacagtccg tcaaggtaac   1140
tccctgctcc tgaattctgc catgcagcca gatctgacag tgagccggac atacagcgga   1200
cccatctgtc tgcaggaccc tctggacaag agctcatga cagagtcctc actctttaac   1260
cctttgtcgg acatcaaagt gaaagtccag agctcgttca tggtttccct gggagtgtct   1320
gagagagctg agtaccacgg caagaatcat tccaggactt ttccccatgg aaacaaccac   1380
agctttagta caatgcatcc cagaaataaa atgccctaca tccaaaatct gtcatcactc   1440
cccacaagga cagaactgag gacaactggt gtctttggcc atttaggggg cgcttagta   1500
atgccaaata caggggtgag cttactcata ccacacggtg ccatcccaga ggagaattct   1560
tgggagattt atatgtccat caaccaaggt gaacccagcc tccagtcaga tggctctgag   1620
gtgctcctga gtcctgaagt cacctgtggt cctccagaca tgatcgtcac cactcccttt   1680
gcattgacca tcccgcactg tgcagatgtc agttctgagc attggaatat ccatttaaag   1740
aagaggacac agcagggcaa atgggaggaa gtgatgtcag tggaagatga atctacatcc   1800
tgttactgcc ttttggaccc ctttgcgtgt catgtgctcc tggacagctt gggacctat   1860
gcgctcactg gagagccaat cacagactgt gccgtgaagc aactgaaggt ggcggttttt   1920
ggctgcatgt cctgtaactc cctggattac aacttgagag tttactgtgt ggacaatacc   1980
ccttgtgcat ttcaggaagt ggtttcagat gaaaggcatc aaggtggaca gctcctggaa   2040
gaaccaaaat tgctgcattt caaagggaat acctttagtc ttcagatttc tgtccttgat   2100
attccccat tcctctggag aattaaacca ttcactgcct gccaggaagt cccgttctcc   2160
cgcgtgtggt gcagtaaccg gcagcccctg cactgtgcct tctccctgga gcgttatacg   2220
cccactacca cccagctgtc ctgcaaaatc tgcattcggc agctcaaagg ccatgaacag   2280
atcctccaag tgcagacatc aatcctagag agtgaacgag aaaccatcac tttcttcgca   2340
caagaggaca gcactttccc tgcacagact ggccccaaag ccttcaaaat tccctactcc   2400
atcagacagc ggatttgtgc tacatttgat accccccaatg ccaaaggcaa ggactggcag   2460
atgttagcac agaaaaacag catcaacagg aatttatctt atttcgctac acaaagtagc   2520
ccatctgctg tcattttgaa cctgtgggaa gctcgtcatc agcatgatgg tgatcttgac   2580
tccctggcct gtgcccttga agagattggg aggacacaca cgaaactctc aaacatttca   2640
gaatcccagc ttgatgaagc cgacttcaac tacagcaggc aaaatggact ctag          2694
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<210> 14
<211> 897
<212> PRT
<213> homo sapiens

<400> 14
Met Gly Arg Ala Ala Ala Thr Ala Gly Gly Gly Gly Gly Ala Arg Arg
1   5   10   15
Trp Leu Pro Trp Leu Gly Leu Cys Phe Trp Ala Ala Gly Thr Ala Ala
            20   25   30
Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
        35   40   45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
    50   55   60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala
65   70   75   80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
                85   90   95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
            100   105   110

16
```

```
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
        115             120             125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
        130             135             140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145             150             155             160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
        165             170             175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
        180             185             190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
        195             200             205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
        210             215             220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225             230             235             240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
            245             250             255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
        260             265             270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
        275             280             285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
        290             295             300
Leu Asp Lys Lys Pro Leu His Glu Ile Lys Pro Gln Ser Ile Glu Asn
305             310             315             320
Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala
            325             330             335
Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser
            340             345             350
Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe
        355             360             365
Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Gly Asn Ser Leu Leu Leu
        370             375             380
Asn Ser Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly
385             390             395             400
Pro Ile Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser
            405             410             415
Ser Leu Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser
        420             425             430
Phe Met Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys
        435             440             445
Asn His Ser Arg Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr
    450             455             460
Met His Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu
465             470             475             480
Pro Thr Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly
            485             490             495
Gly Arg Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His
        500             505             510
Gly Ala Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn
        515             520             525
Gln Gly Glu Pro Ser Leu Gln Ser Asp Gly Ser Glu Val Leu Leu Ser
        530             535             540
Pro Glu Val Thr Cys Gly Pro Pro Asp Met Ile Val Thr Thr Pro Phe
545             550             555             560
```

17

```
Ala Leu Thr Ile Pro His Cys Ala Asp Val Ser Ser Glu His Trp Asn
                565             570             575
Ile His Leu Lys Lys Arg Thr Gln Gln Gly Lys Trp Glu Glu Val Met
                580             585             590
Ser Val Glu Asp Glu Ser Thr Ser Cys Tyr Cys Leu Leu Asp Pro Phe
            595             600             605
Ala Cys His Val Leu Leu Asp Ser Phe Gly Thr Tyr Ala Leu Thr Gly
        610             615             620
Glu Pro Ile Thr Asp Cys Ala Val Lys Gln Leu Lys Val Ala Val Phe
625             630             635             640
Gly Cys Met Ser Cys Asn Ser Leu Asp Tyr Asn Leu Arg Val Tyr Cys
                645             650             655
Val Asp Asn Thr Pro Cys Ala Phe Gln Glu Val Val Ser Asp Glu Arg
                660             665             670
His Gln Gly Gly Gln Leu Leu Glu Glu Pro Lys Leu Leu His Phe Lys
            675             680             685
Gly Asn Thr Phe Ser Leu Gln Ile Ser Val Leu Asp Ile Pro Pro Phe
        690             695             700
Leu Trp Arg Ile Lys Pro Phe Thr Ala Cys Gln Glu Val Pro Phe Ser
705             710             715             720
Arg Val Trp Cys Ser Asn Arg Gln Pro Leu His Cys Ala Phe Ser Leu
                725             730             735
Glu Arg Tyr Thr Pro Thr Thr Thr Gln Leu Ser Cys Lys Ile Cys Ile
            740             745             750
Arg Gln Leu Lys Gly His Glu Gln Ile Leu Gln Val Gln Thr Ser Ile
            755             760             765
Leu Glu Ser Glu Arg Glu Thr Ile Thr Phe Phe Ala Gln Glu Asp Ser
        770             775             780
Thr Phe Pro Ala Gln Thr Gly Pro Lys Ala Phe Lys Ile Pro Tyr Ser
785             790             795             800
Ile Arg Gln Arg Ile Cys Ala Thr Phe Asp Thr Pro Asn Ala Lys Gly
                805             810             815
Lys Asp Trp Gln Met Leu Ala Gln Lys Asn Ser Ile Asn Arg Asn Leu
            820             825             830
Ser Tyr Phe Ala Thr Gln Ser Ser Pro Ser Ala Val Ile Leu Asn Leu
            835             840             845
Trp Glu Ala Arg His Gln His Asp Gly Asp Leu Asp Ser Leu Ala Cys
        850             855             860
Ala Leu Glu Glu Ile Gly Arg Thr His Thr Lys Leu Ser Asn Ile Ser
865             870             875             880
Glu Ser Gln Leu Asp Glu Ala Asp Phe Asn Tyr Ser Arg Gln Asn Gly
        885             890             895
Leu
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<210> 15
<211> 2661
<212> DNA
<213> homo sapiens

<400> 15
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atggggagag cggcggccac cgcaggcggc ggcggagggg cgcgccgctg gctcccgtgg    60
ctggggctgt gcttctgggc ggcagggacc gcggctgccc gaggaactga caatggcgaa   120
gcccttcccg aatccatccc atcagctcct gggacactgc ctcatttcat agaggagcca   180
gatgatgctt atattatcaa gagcaaccct attgcactca ggtgcaaagc gaggccagcc   240
atgcagatat tcttcaaatg caacggcgag tgggtccatc agaacgagca cgtctctgaa   300
```

```
gagactctgg acgagagctc aggtttgaag gtccgcgaag tgttcatcaa tgttactagg     360
caacaggtgg aggacttcca tgggcccgag gactattggt gccagtgtgt ggcgtggagc     420
cacctgggta cctccaagag caggaaggcc tctgtgcgca tagcctattt acggaaaaac     480
tttgaacaag acccacaagg aagggaagtt cccattgaag gcatgattgt actgcactgc     540
cgcccaccag agggagtccc tgctgccgag gtggaatggc tgaaaaatga agagcccatt     600
gactctgaac aagacgagaa cattgacacc agggctgacc ataacctgat catcaggcag     660
gcacggctct cggactcagg aaattacacc tgcatggcag ccaacatcgt ggctaagagg     720
agaagcctgt cggccactgt tgtggtctac gtggatggga ctgggaagt gtggagcgaa     780
tggtccgtct gcagtccaga gtgtgaacat ttgcggatcc gggagtgcac agcaccaccc     840
ccgagaaatg ggggcaaatt ctgtgaaggt ctaagccagg aatctgaaaa ctgcacagat     900
ggtctttgca tcctaggcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt     960
gctgccgtcg tggccgttgc agtcctggtc attggtgtca ccctttacag acggagccag    1020
agtgactatg gcgtggacgt cattgactct ctgcattga caggtggctt ccagaccttc    1080
aacttcaaaa cagtccgtca aggtaactcc ctgctcctga attctgccat gcagccagat    1140
ctgacagtga gccggacata cagcggaccc atctgtctgc aggaccctct ggacaaggag    1200
ctcatgacag agtcctcact ctttaaccct ttgtcggaca tcaaagtgaa agtccagagc    1260
tcgttcatgg tttccctggg agtgtctgag agagctgagt accacggcaa gaatcattcc    1320
aggactttc cccatggaaa caaccacagc tttagtacaa tgcatcccag aaataaaatg    1380
ccctacatcc aaaatctgtc atcactcccc acaaggacag aactgaggac aactggtgtc    1440
tttggccatt tagggggggcg cttagtaatg ccaaatacag gggtgagctt actcatacca    1500
cacggtgcca tcccagagga gaattcttgg gagatttata tgtccatcaa ccaaggtgaa    1560
cccagcctcc agtcagatgg ctctgaggtg ctcctgagtc ctgaagtcac ctgtggtcct    1620
ccagacatga tcgtcaccac tcccttttgca ttgaccatcc cgcactgtgc agatgtcagt    1680
tctgagcatt ggaatatcca tttaaagaag aggacacagc agggcaaatg ggaggaagtg    1740
atgtcagtgg aagatgaatc tacatcctgt tactgccttt tggaccccctt tgcgtgtcat    1800
gtgctcctgg acagctttgg gacctatgcg ctcactggag agccaatcac agactgtgcc    1860
gtgaagcaac tgaaggtggc ggttttggc tgcatgtcct gtaactccct ggattacaac    1920
ttgagagttt actgtgtgga cataccccct tgtgcatttc aggaagtggt ttcagatgaa    1980
aggcatcaag gtggacagct cctggaagaa ccaaaattgc tgcatttcaa agggaatacc    2040
tttagtcttc agatttctgt ccttgatatt ccccccattcc tctggagaat taaaccattc    2100
actgcctgcc aggaagtccc gttctcccgc gtgtggtgca gtaaccggca gccctgcac    2160
tgtgccttct ccctggagcg ttatacgccc actaccaccc agctgtcctg caaaatctgc    2220
attcggcagc tcaaaggcca tgaacagatc ctccaagtgc agacatcaat cctagagagt    2280
gaacgagaaa ccatcacttt cttcgcacaa gaggacagca ctttccctgc acagactggc    2340
cccaaagcct tcaaaattcc ctactccatc agacagcgga tttgtgctac atttgatacc    2400
cccaatgcca aaggcaagga ctggcagatg ttagcacaga aaaacagcat caacaggaat    2460
ttatcttatt cgctacaca aagtagccca tctgctgtca ttttgaacct gtgggaagct    2520
cgtcatcagc atgatggtga tcttgactcc ctggcctgtg cccttgaaga gattgggagg    2580
acacacacga aactctcaaa catttcagaa tcccagcttg atgaagccga cttcaactac    2640
agcaggcaaa atggactcta g                                              2661
```

<210> 16
<211> 886
<212> PRT
<213> homo sapiens

<400> 16
Met Gly Arg Ala Ala Ala Thr Ala Gly Gly Gly Gly Gly Ala Arg Arg
1   5   10   15
Trp Leu Pro Trp Leu Gly Leu Cys Phe Trp Ala Ala Gly Thr Ala Ala
            20   25   30
Ala Arg Gly Thr Asp Asn Gly Glu Ala Leu Pro Glu Ser Ile Pro Ser
        35   40   45
Ala Pro Gly Thr Leu Pro His Phe Ile Glu Glu Pro Asp Asp Ala Tyr
    50   55   60
Ile Ile Lys Ser Asn Pro Ile Ala Leu Arg Cys Lys Ala Arg Pro Ala

19

```
65                    70                    75                    80
Met Gln Ile Phe Phe Lys Cys Asn Gly Glu Trp Val His Gln Asn Glu
                85                    90                    95
His Val Ser Glu Glu Thr Leu Asp Glu Ser Ser Gly Leu Lys Val Arg
            100                   105                   110
Glu Val Phe Ile Asn Val Thr Arg Gln Gln Val Glu Asp Phe His Gly
           115                   120                   125
Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala Trp Ser His Leu Gly Thr
    130                   135                   140
Ser Lys Ser Arg Lys Ala Ser Val Arg Ile Ala Tyr Leu Arg Lys Asn
145                   150                   155                   160
Phe Glu Gln Asp Pro Gln Gly Arg Glu Val Pro Ile Glu Gly Met Ile
                165                   170                   175
Val Leu His Cys Arg Pro Pro Glu Gly Val Pro Ala Ala Glu Val Glu
            180                   185                   190
Trp Leu Lys Asn Glu Glu Pro Ile Asp Ser Glu Gln Asp Glu Asn Ile
            195                   200                   205
Asp Thr Arg Ala Asp His Asn Leu Ile Ile Arg Gln Ala Arg Leu Ser
    210                   215                   220
Asp Ser Gly Asn Tyr Thr Cys Met Ala Ala Asn Ile Val Ala Lys Arg
225                   230                   235                   240
Arg Ser Leu Ser Ala Thr Val Val Val Tyr Val Asp Gly Ser Trp Glu
                245                   250                   255
Val Trp Ser Glu Trp Ser Val Cys Ser Pro Glu Cys Glu His Leu Arg
            260                   265                   270
Ile Arg Glu Cys Thr Ala Pro Pro Pro Arg Asn Gly Gly Lys Phe Cys
            275                   280                   285
Glu Gly Leu Ser Gln Glu Ser Glu Asn Cys Thr Asp Gly Leu Cys Ile
    290                   295                   300
Leu Gly Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr Ser Gly Leu Gly
305                   310                   315                   320
Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly Val Thr Leu Tyr
                325                   330                   335
Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile Asp Ser Ser Ala
            340                   345                   350
Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr Val Arg Gln Gly
            355                   360                   365
Asn Ser Leu Leu Leu Asn Ser Ala Met Gln Pro Asp Leu Thr Val Ser
    370                   375                   380
Arg Thr Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro Leu Asp Lys Glu
385                   390                   395                   400
Leu Met Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser Asp Ile Lys Val
                405                   410                   415
Lys Val Gln Ser Ser Phe Met Val Ser Leu Gly Val Ser Glu Arg Ala
            420                   425                   430
Glu Tyr His Gly Lys Asn His Ser Arg Thr Phe Pro His Gly Asn Asn
            435                   440                   445
His Ser Phe Ser Thr Met His Pro Arg Asn Lys Met Pro Tyr Ile Gln
    450                   455                   460
Asn Leu Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg Thr Thr Gly Val
465                   470                   475                   480
Phe Gly His Leu Gly Gly Arg Leu Val Met Pro Asn Thr Gly Val Ser
                485                   490                   495
Leu Leu Ile Pro His Gly Ala Ile Pro Glu Glu Asn Ser Trp Glu Ile
            500                   505                   510
Tyr Met Ser Ile Asn Gln Gly Glu Pro Ser Leu Gln Ser Asp Gly Ser

                            20
```

Glu Val Leu Leu Ser Pro Glu Val Thr Cys Gly Pro Pro Asp Met Ile
530   535   540
Val Thr Thr Pro Phe Ala Leu Thr Ile Pro His Cys Ala Asp Val Ser
545   550   555   560
Ser Glu His Trp Asn Ile His Leu Lys Lys Arg Thr Gln Gln Gly Lys
                         565   570   575
Trp Glu Glu Val Met Ser Val Glu Asp Glu Ser Thr Ser Cys Tyr Cys
                         580   585   590
Leu Leu Asp Pro Phe Ala Cys His Val Leu Leu Asp Ser Phe Gly Thr
                         595   600   605
Tyr Ala Leu Thr Gly Glu Pro Ile Thr Asp Cys Ala Val Lys Gln Leu
610   615   620
Lys Val Ala Val Phe Gly Cys Met Ser Cys Asn Ser Leu Asp Tyr Asn
625   630   635   640
Leu Arg Val Tyr Cys Val Asp Asn Thr Pro Cys Ala Phe Gln Glu Val
                         645   650   655
Val Ser Asp Glu Arg His Gln Gly Gly Gln Leu Leu Glu Glu Pro Lys
                         660   665   670
Leu Leu His Phe Lys Gly Asn Thr Phe Ser Leu Gln Ile Ser Val Leu
                         675   680   685
Asp Ile Pro Pro Phe Leu Trp Arg Ile Lys Pro Phe Thr Ala Cys Gln
690   695   700
Glu Val Pro Phe Ser Arg Val Trp Cys Ser Asn Arg Gln Pro Leu His
705   710   715   720
Cys Ala Phe Ser Leu Glu Arg Tyr Thr Pro Thr Thr Thr Gln Leu Ser
                         725   730   735
Cys Lys Ile Cys Ile Arg Gln Leu Lys Gly His Glu Gln Ile Leu Gln
                         740   745   750
Val Gln Thr Ser Ile Leu Glu Ser Glu Arg Glu Thr Ile Thr Phe Phe
                         755   760   765
Ala Gln Glu Asp Ser Thr Phe Pro Ala Gln Thr Gly Pro Lys Ala Phe
770   775   780
Lys Ile Pro Tyr Ser Ile Arg Gln Arg Ile Cys Ala Thr Phe Asp Thr
785   790   795   800
Pro Asn Ala Lys Gly Lys Asp Trp Gln Met Leu Ala Gln Lys Asn Ser
                         805   810   815
Ile Asn Arg Asn Leu Ser Tyr Phe Ala Thr Gln Ser Ser Pro Ser Ala
                         820   825   830
Val Ile Leu Asn Leu Trp Glu Ala Arg His Gln His Asp Gly Asp Leu
                         835   840   845
Asp Ser Leu Ala Cys Ala Leu Glu Glu Ile Gly Arg Thr His Thr Lys
850   855   860
Leu Ser Asn Ile Ser Glu Ser Gln Leu Asp Glu Ala Asp Phe Asn Tyr
865   870   875   880
Ser Arg Gln Asn Gly Leu
                         885

<210> 17
<211> 1041
<212> DNA
<213> homo sapiens

<400> 17
atggcagcca acatcgtggc taagaggaga agcctgtcgg ccactgttgt ggtctacgtg   60
gatgggagct gggaagtgtg gagcgaatgg tccgtctgca gtccagagtg tgaacatttg   120

21

```
cggatccggg agtgcacagc accacccccg agaaatgggg gcaaattctg tgaaggtcta    180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc tagataaaaa acctcttcat    240
gaaataaaac cccaaagcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt    300
gctgccgtcg tggccgttgc agtcctggtc attggtgtca ccctttacag acggagccag    360
agtgactatg gcgtggacgt cattgactct tctgcattga caggtggctt ccagaccttc    420
aacttcaaaa cagtccgtca agccaagaat atcatggaac taatgataca agaaaaatcc    480
tttggtaact ccctgctcct gaattctgcc atgcagccag atctgacagt gagccggaca    540
tacagcggac ccatctgtct gcaggaccct ctggacaagg agctcatgac agagtcctca    600
ctctttaacc ctttgtcgga catcaaagtg aaagtccaga gctcgttcat ggtttccctg    660
ggagtgtctg agagagctga gtaccacggc aagaatcatt ccaggacttt tccccatgga    720
aacaaccaca gctttagtac aatgcatccc agaaataaaa tgccctacat ccaaaatctg    780
tcatcactcc ccacaaggac agaactgagg acaactggtg tctttggcca tttagggggg    840
cgcttagtaa tgccaaatac aggggtgagc ttactcatac cacacggtgc catcccagag    900
gagaattctt gggagattta tatgtccatc aaccaaggtg aacccagtga aaatccagca    960
aacaaaggat caaatagctt gttgaagaac acatatgcca ttggggggaaa aataagcaga   1020
catctgggtt cttctcgctg a                                             1041
```

<210> 18
<211> 346
<212> PRT
<213> homo sapiens

<400> 18
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Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
1               5                   10                  15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
            20                  25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
            35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
        50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Asp Lys Lys Pro Leu His
65                  70                  75                  80
Glu Ile Lys Pro Gln Ser Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr
                85                  90                  95
Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly
            100                 105                 110
Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile
            115                 120                 125
Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr
        130                 135                 140
Val Arg Gln Ala Lys Asn Ile Met Glu Leu Met Ile Gln Glu Lys Ser
145                 150                 155                 160
Phe Gly Asn Ser Leu Leu Leu Asn Ser Ala Met Gln Pro Asp Leu Thr
                165                 170                 175
Val Ser Arg Thr Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro Leu Asp
            180                 185                 190
Lys Glu Leu Met Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser Asp Ile
            195                 200                 205
Lys Val Lys Val Gln Ser Ser Phe Met Val Ser Leu Gly Val Ser Glu
        210                 215                 220
Arg Ala Glu Tyr His Gly Lys Asn His Ser Arg Thr Phe Pro His Gly
225                 230                 235                 240
Asn Asn His Ser Phe Ser Thr Met His Pro Arg Asn Lys Met Pro Tyr
                245                 250                 255
Ile Gln Asn Leu Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg Thr Thr
```

22
```

```
                    260                  265                  270
Gly Val Phe Gly His Leu Gly Gly Arg Leu Val Met Pro Asn Thr Gly
            275                  280                  285
Val Ser Leu Leu Ile Pro His Gly Ala Ile Pro Glu Glu Asn Ser Trp
        290                  295                  300
Glu Ile Tyr Met Ser Ile Asn Gln Gly Glu Pro Ser Glu Asn Pro Ala
305                  310                  315                  320
Asn Lys Gly Ser Asn Ser Leu Leu Lys Asn Thr Tyr Ala Ile Gly Gly
                325                  330                  335
Lys Ile Ser Arg His Leu Gly Ser Ser Arg
            340                  345
```

<210> 19
<211> 1008
<212> DNA
<213> homo sapiens

<400> 19
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atggcagcca acatcgtggc taagaggaga agcctgtcgg ccactgttgt ggtctacgtg      60
gatgggagct gggaagtgtg gagcgaatgg tccgtctgca gtccagagtg tgaacatttg     120
cggatccggg agtgcacagc accaccccccg agaaatgggg gcaaattctg tgaaggtcta     180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc taggcattga gaatgccagc     240
gacattgctt tgtactcggg cttgggtgct gccgtcgtgg ccgttgcagt cctggtcatt     300
ggtgtcaccc tttacagacg gagccagagt gactatggcg tggacgtcat tgactcttct     360
gcattgacag gtggcttcca gaccttcaac ttcaaaacag tccgtcaagc caagaatatc     420
atggaactaa tgatacaaga aaaatccttt ggtaactccc tgctcctgaa ttctgccatg     480
cagccagatc tgacagtgag ccggacatac agcggaccca tctgtctgca ggaccctctg     540
gacaaggagc tcatgacaga gtcctcactc tttaaccctt tgtcggacat caaagtgaaa     600
gtccagagct cgttcatggt ttccctggga gtgtctgaga gagctgagta ccacggcaag     660
aatcattcca ggactttttcc ccatggaaac aaccacagct ttagtacaat gcatcccaga     720
aataaaatgc cctacatcca aaatctgtca tcactcccca caaggacaga actgaggaca     780
actggtgtct ttggccattt aggggggcgc ttagtaatgc caaatacagg ggtgagctta     840
ctcataccac acggtgccat cccagaggag aattcttggg agatttatat gtccatcaac     900
caaggtgaac ccagtgaaaa tccagcaaac aaaggatcaa atagcttgtt gaagaacaca     960
tatgccattg ggggaaaaat aagcagacat ctgggttctt ctcgctga               1008
```

<210> 20
<211> 335
<212> PRT
<213> homo sapiens

<400> 20
```
Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
1               5                   10                  15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
            20                  25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
        35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
    50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Gly Ile Glu Asn Ala Ser
65                  70                  75                  80
Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala
            85                  90                  95
Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr
        100                 105                 110
```

23

```
Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr
        115                 120                 125
Phe Asn Phe Lys Thr Val Arg Gln Ala Lys Asn Ile Met Glu Leu Met
    130                 135                 140
Ile Gln Glu Lys Ser Phe Gly Asn Ser Leu Leu Leu Asn Ser Ala Met
145                 150                 155                 160
Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile Cys Leu
                165                 170                 175
Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu Phe Asn
            180                 185                 190
Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met Val Ser
        195                 200                 205
Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His Ser Arg
    210                 215                 220
Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr Met His Pro Arg
225                 230                 235                 240
Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr Arg Thr
                245                 250                 255
Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg Leu Val
            260                 265                 270
Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala Ile Pro
        275                 280                 285
Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly Glu Pro
    290                 295                 300
Ser Glu Asn Pro Ala Asn Lys Gly Ser Asn Ser Leu Leu Lys Asn Thr
305                 310                 315                 320
Tyr Ala Ile Gly Gly Lys Ile Ser Arg His Leu Gly Ser Ser Arg
                325                 330                 335


<210> 21
<211> 999
<212> DNA
<213> homo sapiens

<400> 21
atggcagcca acatcgtggc taagaggaga agcctgtcgg ccactgttgt ggtctacgtg      60
gatgggagct gggaagtgtg gagcgaatgg tccgtctgca gtccagagtg tgaacatttg     120
cggatccggg agtgcacagc accaccccg agaaatgggg gcaaattctg tgaaggtcta      180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc tagataaaaa acctcttcat     240
gaaataaaac cccaaagcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt     300
gctgccgtcg tggccgttgc agtcctggtc attggtgtca cccttacag acggagccag      360
agtgactatg cgtggacgt cattgactct ctgcattga caggtggctt ccagaccttc       420
aacttcaaaa cagtccgtca aggtaactcc ctgctcctga ttctgccat gcagccagat      480
ctgacagtga ccggacata cagcggaccc atctgtctgc aggaccctct ggacaaggag      540
ctcatgacag agtcctcact ctttaaccct ttgtcggaca tcaaagtgaa agtccagagc     600
tcgttcatgg tttccctggg agtgtctgag agagctgagt accacggcaa gaatcattcc     660
aggactttc cccatggaaa caaccacagc tttagtacaa tgcatcccag aaataaaatg       720
ccctacatcc aaaatctgtc atcactcccc acaaggacag aactgaggac aactggtgtc     780
tttggccatt taggggggcg cttagtaatg ccaaatacag gggtgagctt actcatacca     840
cacggtgcca tcccagagga gaattcttgg gagatttata tgtccatcaa ccaaggtgaa     900
cccagtgaaa atccagcaaa caaaggatca aatagcttgt tgaagaacac atatgccatt     960
gggggaaaaa taagcagaca tctgggttct ctcgctga                            999


<210> 22
<211> 332
<212> PRT
```

24

<210> homo sapiens

<400> 22
```
Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
1               5                   10                  15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
            20                  25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
        35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
    50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Asp Lys Lys Pro Leu His
65                  70                  75                  80
Glu Ile Lys Pro Gln Ser Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr
                85                  90                  95
Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly
            100                 105                 110
Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile
            115                 120                 125
Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr
    130                 135                 140
Val Arg Gln Gly Asn Ser Leu Leu Leu Asn Ser Ala Met Gln Pro Asp
145                 150                 155                 160
Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro
                165                 170                 175
Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser
            180                 185                 190
Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met Val Ser Leu Gly Val
            195                 200                 205
Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His Ser Arg Thr Phe Pro
    210                 215                 220
His Gly Asn Asn His Ser Phe Ser Thr Met His Pro Arg Asn Lys Met
225                 230                 235                 240
Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg
                245                 250                 255
Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg Leu Val Met Pro Asn
            260                 265                 270
Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala Ile Pro Glu Glu Asn
    275                 280                 285
Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly Glu Pro Ser Glu Asn
    290                 295                 300
Pro Ala Asn Lys Gly Ser Asn Ser Leu Leu Lys Asn Thr Tyr Ala Ile
305                 310                 315                 320
Gly Gly Lys Ile Ser Arg His Leu Gly Ser Ser Arg
                325                 330
```

<210> 23
<211> 966
<212> DNA
<213> homo sapiens

<400> 23
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atggcagcca acatcgtggc taagaggaga agcctgtcgg ccactgttgt ggtctacgtg      60
gatgggagct gggaagtgtg gagcgaatgg tccgtctgca gtccagagtg tgaacatttg     120
cggatccggg agtgcacagc accacccccg agaaatgggg gcaaattctg tgaaggtcta     180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc taggcattga gaatgccagc     240
```

```
gacattgctt tgtactcggg cttgggtgct gccgtcgtgg ccgttgcagt cctggtcatt      300
ggtgtcaccc tttacagacg gagccagagt gactatggcg tggacgtcat tgactcttct      360
gcattgacag gtggcttcca gaccttcaac ttcaaaacag tccgtcaagg taactccctg      420
ctcctgaatt ctgccatgca gccagatctg acagtgagcc ggacatacag cggacccatc      480
tgtctgcagg accctctgga caaggagctc atgacagagt cctcactctt taacccctttg     540
tcggacatca aagtgaaagt ccagagctcg ttcatggttt ccctgggagt gtctgagaga      600
gctgagtacc acggcaagaa tcattccagg acttttcccc atggaaacaa ccacagcttt      660
agtacaatgc atcccagaaa taaatgccc tacatccaaa atctgtcatc actccccaca       720
aggacagaac tgaggacaac tggtgtcttt ggccatttag gggggcgctt agtaatgcca      780
aatacagggg tgagcttact cataccacac ggtgccatcc cagaggagaa ttcttgggag      840
atttatatgt ccatcaacca aggtgaaccc agtgaaaatc cagcaaacaa aggatcaaat      900
agcttgttga agaacacata tgccattggg ggaaaaataa gcagacatct gggttcttct      960
cgctga                                                                 966
```

```
<210> 24
<211> 321
<212> PRT
<213> homo sapiens
```

```
<400> 24
Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
1               5                   10                  15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
            20                  25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
            35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
    50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Gly Ile Glu Asn Ala Ser
65                  70                  75                  80
Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala
                85                  90                  95
Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr
            100                 105                 110
Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr
            115                 120                 125
Phe Asn Phe Lys Thr Val Arg Gln Gly Asn Ser Leu Leu Leu Asn Ser
    130                 135                 140
Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile
145                 150                 155                 160
Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu
                165                 170                 175
Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met
                180                 185                 190
Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His
        195                 200                 205
Ser Arg Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr Met His
    210                 215                 220
Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr
225                 230                 235                 240
Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg
                245                 250                 255
Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala
            260                 265                 270
Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly
    275                 280                 285
```

26

```
Glu Pro Ser Glu Asn Pro Ala Asn Lys Gly Ser Asn Ser Leu Leu Lys
    290                 295                 300

Asn Thr Tyr Ala Ile Gly Gly Lys Ile Ser Arg His Leu Gly Ser Ser
305                 310                 315                 320

Arg
```

<210> 25
<211> 2043
<212> DNA
<213> homo sapiens

<400> 25

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atggcagcca acatcgtggc taagaggaga agcctgtcgg ccactgttgt ggtctacgtg      60
gatgggagct gggaagtgtg gagcgaatgg tccgtctgca gtccagagtg tgaacatttg     120
cggatccggg agtgcacagc accacc+ccg agaaatgggg gcaaattctg tgaaggtcta     180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc tagataaaaa acctcttcat     240
gaaataaaac cccaaagcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt     300
gctgccgtcg tggccgttgc agtcctggtc attggtgtca ccctttacag acggagccag     360
agtgactatg gcgtggacgt cattgactct tctgcattga caggtggctt ccagaccttc     420
aacttcaaaa cagtccgtca agccaagaat atcatggaac taatgataca agaaaaatcc     480
tttggtaact ccctgctcct gaattctgcc atgcagccag atctgacagt gagccggaca     540
tacagcggac ccatctgtct gcaggaccct ctggacaagg agctcatgac agagtcctca     600
ctctttaacc ctttgtcgga catcaaagtg aaagtccaga gctcgttcat ggtttccctg     660
ggagtgtctg agagagctga gtaccacggc aagaatcatt ccaggacttt tccccatgga     720
aacaaccaca gctttagtac aatgcatccc agaaataaaa tgccctacat ccaaaatctg     780
tcatcactcc ccacaaggac agaactgagg acaactggtg tctttggcca tttaggggg     840
cgcttagtaa tgccaaatac aggggtgagc ttactcatac cacacggtgc catcccagag     900
gagaattctt gggagattta tatgtccatc aaccaaggtg aacccagcct ccagtcagat     960
ggctctgagg tgctcctgag tcctgaagtc acctgtggtc ctccagacat gatcgtcacc    1020
actccctttg cattgaccat cccgcactgt gcagatgtca gttctgagca ttggaatatc    1080
catttaaaga agaggacaca gcagggcaaa tgggaggaag tgatgtcagt ggaagatgaa    1140
tctacatcct gttactgcct tttggacccc tttgcgtgtc atgtgctcct ggacagcttt    1200
gggacctatg cgctcactgg agagccaatc acagactgtg ccgtgaagca actgaaggtg    1260
gcggtttttg gctgcatgtc ctgtaactcc ctggattaca acttgagagt ttactgtgtg    1320
gacaataccc cttgtgcatt tcaggaagtg gtttcagatg aaaggcatca aggtggacag    1380
ctcctggaag aaccaaaatt gctgcatttc aaagggaata cctttagtct tcagatttct    1440
gtccttgata ttcccccatt cctctggaga attaaaccat tcactgcctg ccaggaagtc    1500
ccgttctccc gcgtgtggtg cagtaaccgg cagcccctgc actgtgcctt ctccctggag    1560
cgttatacgc ccactaccac ccagctgtcc tgcaaaatct gcattcggca gctcaaaggc    1620
catgaacaga tcctccaagt gcagacatca atcctagaga gtgaacgaga aaccatcact    1680
ttcttcgcac aagaggacag cactttccct gcacagactg gccccaaagc cttcaaaatt    1740
ccctactcca tcagacagcg gatttgtgct acatttgata cccccaatgc caaaggcaag    1800
gactggcaga tgttagcaca gaaaaacagc atcaacagga atttatctta tttcgctaca    1860
caaagtagcc catctgctgt cattttgaac ctgtgggaag ctcgtcatca gcatgatggt    1920
gatcttgact ccctggcctg tgcccttgaa gagattggga ggacacacac gaaactctca    1980
aacatttcag aatcccagct tgatgaagcc gacttcaact acagcaggca aaatggactc    2040
tag                                                                  2043
```

<210> 26
<211> 680
<212> PRT
<213> homo sapiens

<400> 26
```
Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
```

```
1                    5                              10                             15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
              20                      25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
          35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
      50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Asp Lys Lys Pro Leu His
65                  70                  75                      80
Glu Ile Lys Pro Gln Ser Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr
              85                  90                  95
Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly
          100                 105                 110
Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile
      115                 120                 125
Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr
      130                 135                 140
Val Arg Gln Ala Lys Asn Ile Met Glu Leu Met Ile Gln Glu Lys Ser
145                 150                 155                 160
Phe Gly Asn Ser Leu Leu Leu Asn Ser Ala Met Gln Pro Asp Leu Thr
              165                 170                 175
Val Ser Arg Thr Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro Leu Asp
          180                 185                 190
Lys Glu Leu Met Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser Asp Ile
          195                 200                 205
Lys Val Lys Val Gln Ser Ser Phe Met Val Ser Leu Gly Val Ser Glu
      210                 215                 220
Arg Ala Glu Tyr His Gly Lys Asn His Ser Arg Thr Phe Pro His Gly
225                 230                 235                 240
Asn Asn His Ser Phe Ser Thr Met His Pro Arg Asn Lys Met Pro Tyr
              245                 250                 255
Ile Gln Asn Leu Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg Thr Thr
          260                 265                 270
Gly Val Phe Gly His Leu Gly Gly Arg Leu Val Met Pro Asn Thr Gly
          275                 280                 285
Val Ser Leu Leu Ile Pro His Gly Ala Ile Pro Glu Glu Asn Ser Trp
      290                 295                 300
Glu Ile Tyr Met Ser Ile Asn Gln Gly Glu Pro Ser Leu Gln Ser Asp
305                 310                 315                 320
Gly Ser Glu Val Leu Leu Ser Pro Glu Val Thr Cys Gly Pro Pro Asp
              325                 330                 335
Met Ile Val Thr Thr Pro Phe Ala Leu Thr Ile Pro His Cys Ala Asp
              340                 345                 350
Val Ser Ser Glu His Trp Asn Ile His Leu Lys Lys Arg Thr Gln Gln
          355                 360                 365
Gly Lys Trp Glu Glu Val Met Ser Val Glu Asp Glu Ser Thr Ser Cys
      370                 375                 380
Tyr Cys Leu Leu Asp Pro Phe Ala Cys His Val Leu Leu Asp Ser Phe
385                 390                 395                 400
Gly Thr Tyr Ala Leu Thr Gly Glu Pro Ile Thr Asp Cys Ala Val Lys
              405                 410                 415
Gln Leu Lys Val Ala Val Phe Gly Cys Met Ser Cys Asn Ser Leu Asp
          420                 425                 430
Tyr Asn Leu Arg Val Tyr Cys Val Asp Asn Thr Pro Cys Ala Phe Gln
          435                 440                 445
Glu Val Val Ser Asp Glu Arg His Gln Gly Gly Gln Leu Leu Glu Glu
```

28

```
          450                         455                         460
Pro Lys Leu Leu His Phe Lys Gly Asn Thr Phe Ser Leu Gln Ile Ser
465                         470                         475                         480
Val Leu Asp Ile Pro Pro Phe Leu Trp Arg Ile Lys Pro Phe Thr Ala
                        485                         490                         495
Cys Gln Glu Val Pro Phe Ser Arg Val Trp Cys Ser Asn Arg Gln Pro
                    500                         505                         510
Leu His Cys Ala Phe Ser Leu Glu Arg Tyr Thr Pro Thr Thr Thr Gln
        515                         520                         525
Leu Ser Cys Lys Ile Cys Ile Arg Gln Leu Lys Gly His Glu Gln Ile
    530                         535                         540
Leu Gln Val Gln Thr Ser Ile Leu Glu Ser Glu Arg Glu Thr Ile Thr
545                         550                         555                         560
Phe Phe Ala Gln Glu Asp Ser Thr Phe Pro Ala Gln Thr Gly Pro Lys
                    565                         570                         575
Ala Phe Lys Ile Pro Tyr Ser Ile Arg Gln Arg Ile Cys Ala Thr Phe
                580                         585                         590
Asp Thr Pro Asn Ala Lys Gly Lys Asp Trp Gln Met Leu Ala Gln Lys
                595                         600                         605
Asn Ser Ile Asn Arg Asn Leu Ser Tyr Phe Ala Thr Gln Ser Ser Pro
    610                         615                         620
Ser Ala Val Ile Leu Asn Leu Trp Glu Ala Arg His Gln His Asp Gly
625                         630                         635                         640
Asp Leu Asp Ser Leu Ala Cys Ala Leu Glu Glu Ile Gly Arg Thr His
                645                         650                         655
Thr Lys Leu Ser Asn Ile Ser Glu Ser Gln Leu Asp Glu Ala Asp Phe
                660                         665                         670
Asn Tyr Ser Arg Gln Asn Gly Leu
        675                         680


<210> 27
<211> 2010
<212> DNA
<213> homo sapiens


<400> 27
atggcagcca  acatcgtggc  taagaggaga  agcctgtcgg  ccactgttgt  ggtctacgtg       60
gatgggagct  gggaagtgtg  gagcgaatgg  tccgtctgca  gtccagagtg  tgaacatttg      120
cggatccggg  agtgcacagc  accacccccg  agaaatgggg  gcaaattctg  tgaaggtcta      180
agccaggaat  ctgaaaactg  cacagatggt  ctttgcatcc  taggcattga  gaatgccagc      240
gacattgctt  tgtactcggg  cttgggtgct  gccgtcgtgg  ccgttgcagt  cctggtcatt      300
ggtgtcaccc  tttacagacg  gagccagagt  gactatggcg  tggacgtcat  tgactcttct      360
gcattgacag  gtggcttcca  gaccttcaac  ttcaaaacag  tccgtcaagc  caagaatatc      420
atggaactaa  tgatacaaga  aaaatccttt  ggtaactccc  tgctcctgaa  ttctgccatg      480
cagccagatc  tgacagtgag  ccggacatac  agcggaccca  tctgtctgca  ggacctctg       540
gacaaggagc  tcatgacaga  gtcctcactc  tttaacccntt  tgtcggacat  caaagtgaaa      600
gtccagagct  cgttcatggt  ttccctggga  gtgtctgaga  gagctgagta  ccacggcaag      660
aatcattcca  ggactttttcc  ccatggaaac  aaccacagct  ttagtacaat  gcatcccaga      720
aataaaatgc  cctacatcca  aaatctgtca  tcactcccca  caaggacaga  actgaggaca      780
actggtgtct  ttggccattt  agggggggcgc  ttagtaatgc  caaatacagg  ggtgagctta      840
ctcataccac  acggtgccat  cccagaggag  aattcttggg  agatttatat  gtccatcaac      900
caaggtgaac  ccagcctcca  gtcagatggc  tctgaggtgc  tcctgagtcc  tgaagtcacc      960
tgtggtcctc  cagacatgat  cgtcaccact  cccttgcat  tgaccatccc  gcactgtgca     1020
gatgtcagtt  ctgagcattg  gaatatccat  ttaaagaaga  ggacacagca  gggcaaatgg     1080
gaggaagtga  tgtcagtgga  agatgaatct  acatcctgtt  actgccttt  ggaccccttt     1140
gcgtgtcatg  tgctcctgga  cagctttggg  acctatgcgc  tcactggaga  gccaatcaca     1200
```

29

```
gactgtgccg tgaagcaact gaaggtggcg gtttttggct gcatgtcctg taactccctg      1260
gattacaact tgagagttta ctgtgtggac aatacccctt gtgcatttca ggaagtggtt      1320
tcagatgaaa ggcatcaagg tggacagctc ctggaagaac caaaattgct gcatttcaaa      1380
gggaatacct ttagtcttca gatttctgtc cttgatattc ccccattcct ctggagaatt      1440
aaaccattca ctgcctgcca ggaagtcccg ttctcccgcg tgtggtgcag taaccggcag      1500
cccctgcact gtgccttctc cctggagcgt tatacgccca ctaccaccca gctgtcctgc      1560
aaaatctgca ttcggcagct caaaggccat gaacagatcc tccaagtgca gacatcaatc      1620
ctagagagtg aacgagaaac catcactttc ttcgcacaag aggacagcac tttccctgca      1680
cagactggcc ccaaagcctt caaaattccc tactccatca gacagcggat ttgtgctaca      1740
tttgataccc ccaatgccaa aggcaaggac tggcagatgt tagcacagaa aaacagcatc      1800
aacaggaatt tatcttattt cgctacacaa agtagcccat ctgctgtcat tttgaacctg      1860
tgggaagctc gtcatcagca tgatggtgat cttgactccc tggcctgtgc ccttgaagag      1920
attgggagga cacacgaa actctcaaac atttcagaat cccagcttga tgaagccgac        1980
ttcaactaca gcaggcaaaa tggactctag                                      2010
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<210> 28
<211> 669
<212> PRT
<213> homo sapiens

<400> 28
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Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
  1               5                  10                  15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
           20                  25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
           35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
       50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Gly Ile Glu Asn Ala Ser
65                  70                  75                  80
Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala
               85                  90                  95
Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr
           100                 105                 110
Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr
           115                 120                 125
Phe Asn Phe Lys Thr Val Arg Gln Ala Lys Asn Ile Met Glu Leu Met
       130                 135                 140
Ile Gln Glu Lys Ser Phe Gly Asn Ser Leu Leu Leu Asn Ser Ala Met
145                 150                 155                 160
Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile Cys Leu
               165                 170                 175
Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu Phe Asn
           180                 185                 190
Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met Val Ser
           195                 200                 205
Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His Ser Arg
       210                 215                 220
Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr Met His Pro Arg
225                 230                 235                 240
Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr Arg Thr
               245                 250                 255
Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg Leu Val
           260                 265                 270
Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala Ile Pro
```

30
```

```
                275                    280                    285
Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly Glu Pro
    290                    295                    300
Ser Leu Gln Ser Asp Gly Ser Glu Val Leu Leu Ser Pro Glu Val Thr
305                    310                    315                    320
Cys Gly Pro Pro Asp Met Ile Val Thr Thr Pro Phe Ala Leu Thr Ile
                325                    330                    335
Pro His Cys Ala Asp Val Ser Ser Glu His Trp Asn Ile His Leu Lys
                340                    345                    350
Lys Arg Thr Gln Gln Gly Lys Trp Glu Glu Val Met Ser Val Glu Asp
                355                    360                    365
Glu Ser Thr Ser Cys Tyr Cys Leu Leu Asp Pro Phe Ala Cys His Val
    370                    375                    380
Leu Leu Asp Ser Phe Gly Thr Tyr Ala Leu Thr Gly Glu Pro Ile Thr
385                    390                    395                    400
Asp Cys Ala Val Lys Gln Leu Lys Val Ala Val Phe Gly Cys Met Ser
                405                    410                    415
Cys Asn Ser Leu Asp Tyr Asn Leu Arg Val Tyr Cys Val Asp Asn Thr
                420                    425                    430
Pro Cys Ala Phe Gln Glu Val Val Ser Asp Glu Arg His Gln Gly Gly
                435                    440                    445
Gln Leu Leu Glu Glu Pro Lys Leu Leu His Phe Lys Gly Asn Thr Phe
    450                    455                    460
Ser Leu Gln Ile Ser Val Leu Asp Ile Pro Pro Phe Leu Trp Arg Ile
465                    470                    475                    480
Lys Pro Phe Thr Ala Cys Gln Glu Val Pro Phe Ser Arg Val Trp Cys
                485                    490                    495
Ser Asn Arg Gln Pro Leu His Cys Ala Phe Ser Leu Glu Arg Tyr Thr
                500                    505                    510
Pro Thr Thr Thr Gln Leu Ser Cys Lys Ile Cys Ile Arg Gln Leu Lys
                515                    520                    525
Gly His Glu Gln Ile Leu Gln Val Gln Thr Ser Ile Leu Glu Ser Glu
                530                    535                    540
Arg Glu Thr Ile Thr Phe Phe Ala Gln Glu Asp Ser Thr Phe Pro Ala
545                    550                    555                    560
Gln Thr Gly Pro Lys Ala Phe Lys Ile Pro Tyr Ser Ile Arg Gln Arg
                565                    570                    575
Ile Cys Ala Thr Phe Asp Thr Pro Asn Ala Lys Gly Lys Asp Trp Gln
                580                    585                    590
Met Leu Ala Gln Lys Asn Ser Ile Asn Arg Asn Leu Ser Tyr Phe Ala
    595                    600                    605
Thr Gln Ser Ser Pro Ser Ala Val Ile Leu Asn Leu Trp Glu Ala Arg
    610                    615                    620
His Gln His Asp Gly Asp Leu Asp Ser Leu Ala Cys Ala Leu Glu Glu
625                    630                    635                    640
Ile Gly Arg Thr His Thr Lys Leu Ser Asn Ile Ser Glu Ser Gln Leu
                645                    650                    655
Asp Glu Ala Asp Phe Asn Tyr Ser Arg Gln Asn Gly Leu
                660                    665
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<210> 29
<211> 2001
<212> DNA
<213> homo sapiens

<400> 29

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gatgggagct gggaagtgtg gagcgaatgg tccgtctgca gtccagagtg tgaacatttg     120
cggatccggg agtgcacagc accacccccg agaaatgggg gcaaattctg tgaaggtcta     180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc tagataaaaa acctcttcat     240
gaaataaaac cccaaagcat tgagaatgcc agcgacattg ctttgtactc gggcttgggt     300
gctgccgtcg tggccgttgc agtcctggtc attggtgtca ccctttacag acggagccag     360
agtgactatg gcgtggacgt cattgactct tctgcattga caggtggctt ccagaccttc     420
aacttcaaaa cagtccgtca aggtaactcc ctgctcctga attctgccat gcagccagat     480
ctgacagtga gccggacata cagcggaccc atctgtctgc aggaccctct ggacaaggag     540
ctcatgacag agtcctcact ctttaaccct ttgtcggaca tcaaagtgaa agtccagagc     600
tcgttcatgg tttccctggg agtgtctgag agagctgagt accacggcaa gaatcattcc     660
aggactttc cccatggaaa caaccacagc tttagtacaa tgcatcccag aaataaaatg     720
ccctacatcc aaaatctgtc atcactcccc acaaggacag aactgaggac aactggtgtc     780
tttggccatt taggggggcg cttagtaatg ccaaatacag gggtgagctt actcatacca     840
cacggtgcca tcccagagga gaattcttgg gagatttata tgtccatcaa ccaaggtgaa     900
cccagcctcc agtcagatgg ctctgaggtg ctcctgagtc ctgaagtcac ctgtggtcct     960
ccagacatga tcgtcaccac tcccctttgca ttgaccatcc cgcactgtgc agatgtcagt    1020
tctgagcatt ggaatatcca tttaagaag aggacacagc agggcaaatg ggaggaagtg    1080
atgtcagtgg aagatgaatc tacatcctgt tactgccttt tggaccccctt tgcgtgtcat    1140
gtgctcctgg acagctttgg gacctatgcg ctcactggag agccaatcac agactgtgcc    1200
gtgaagcaac tgaaggtggc ggttttttggc tgcatgtcct gtaactccct ggattacaac    1260
ttgagagttt actgtgtgga caatacccct tgtgcatttc aggaagtggt ttcagatgaa    1320
aggcatcaag gtggacagct cctggaagaa ccaaaattgc tgcatttcaa agggaatacc    1380
tttagtcttc agatttctgt ccttgatatt cccccattcc tctggagaat taaaccattc    1440
actgcctgcc aggaagtccc gttctcccgc gtgtggtgca gtaaccggca gccccctgcac    1500
tgtgccttct ccctggagcg ttatacgccc actaccaccc agctgtcctg caaaatctgc    1560
attcggcagc tcaaaggcca tgaacagatc ctccaagtgc agacatcaat cctagagagt    1620
gaacgagaaa ccatcacttt cttcgcacaa gaggacagca ctttccctgc acagactggc    1680
cccaaagcct tcaaaattcc ctactccatc agacagcgga tttgtgctac atttgatacc    1740
cccaatgcca aaggcaagga ctggcagatg ttagcacaga aaaacagcat caacaggaat    1800
ttatcttatt tcgctacaca aagtagccca tctgctgtca ttttgaacct gtgggaagct    1860
cgtcatcagc atgatggtga tcttgactcc ctggcctgtg cccttgaaga gattgggagg    1920
acacacgga aactctcaaa catttcagaa tcccagcttg atgaagccga cttcaactac    1980
agcaggcaaa atggactcta g                                                2001
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<210> 30
<211> 666
<212> PRT
<213> homo sapiens

<400> 30
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Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
1               5                   10                  15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
            20                  25                  30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
        35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
    50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Asp Lys Lys Pro Leu His
65                  70                  75                  80
Glu Ile Lys Pro Gln Ser Ile Glu Asn Ala Ser Asp Ile Ala Leu Tyr
                85                  90                  95
Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala Val Leu Val Ile Gly
            100                 105                 110
Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr Gly Val Asp Val Ile
```

32

```
            115                    120                      125
Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr Phe Asn Phe Lys Thr
    130                    135                  140
Val Arg Gln Gly Asn Ser Leu Leu Leu Asn Ser Ala Met Gln Pro Asp
145                    150                  155                  160
Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile Cys Leu Gln Asp Pro
                   165                  170                  175
Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu Phe Asn Pro Leu Ser
               180                  185                  190
Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met Val Ser Leu Gly Val
           195                  200                  205
Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His Ser Arg Thr Phe Pro
       210                  215                  220
His Gly Asn Asn His Ser Phe Ser Thr Met His Pro Arg Asn Lys Met
225                  230                  235                  240
Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr Arg Thr Glu Leu Arg
                   245                  250                  255
Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg Leu Val Met Pro Asn
               260                  265                  270
Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala Ile Pro Glu Glu Asn
           275                  280                  285
Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly Glu Pro Ser Leu Gln
       290                  295                  300
Ser Asp Gly Ser Glu Val Leu Leu Ser Pro Glu Val Thr Cys Gly Pro
305                  310                  315                  320
Pro Asp Met Ile Val Thr Thr Pro Phe Ala Leu Thr Ile Pro His Cys
               325                  330                  335
Ala Asp Val Ser Ser Glu His Trp Asn Ile His Leu Lys Lys Arg Thr
           340                  345                  350
Gln Gln Gly Lys Trp Glu Glu Val Met Ser Val Glu Asp Glu Ser Thr
       355                  360                  365
Ser Cys Tyr Cys Leu Leu Asp Pro Phe Ala Cys His Val Leu Leu Asp
   370                  375                  380
Ser Phe Gly Thr Tyr Ala Leu Thr Gly Glu Pro Ile Thr Asp Cys Ala
385                  390                  395                  400
Val Lys Gln Leu Lys Val Ala Val Phe Gly Cys Met Ser Cys Asn Ser
               405                  410                  415
Leu Asp Tyr Asn Leu Arg Val Tyr Cys Val Asp Asn Thr Pro Cys Ala
           420                  425                  430
Phe Gln Glu Val Val Ser Asp Glu Arg His Gln Gly Gly Gln Leu Leu
       435                  440                  445
Glu Glu Pro Lys Leu Leu His Phe Lys Gly Asn Thr Phe Ser Leu Gln
   450                  455                  460
Ile Ser Val Leu Asp Ile Pro Pro Phe Leu Trp Arg Ile Lys Pro Phe
465                  470                  475                  480
Thr Ala Cys Gln Glu Val Pro Phe Ser Arg Val Trp Cys Ser Asn Arg
               485                  490                  495
Gln Pro Leu His Cys Ala Phe Ser Leu Glu Arg Tyr Thr Pro Thr Thr
           500                  505                  510
Thr Gln Leu Ser Cys Lys Ile Cys Ile Arg Gln Leu Lys Gly His Glu
       515                  520                  525
Gln Ile Leu Gln Val Gln Thr Ser Ile Leu Glu Ser Glu Arg Glu Thr
   530                  535                  540
Ile Thr Phe Phe Ala Gln Glu Asp Ser Thr Phe Pro Ala Gln Thr Gly
545                  550                  555                  560
Pro Lys Ala Phe Lys Ile Pro Tyr Ser Ile Arg Gln Arg Ile Cys Ala
```

33

```
                     565                  570                  575
Thr Phe Asp Thr Pro Asn Ala Lys Gly Lys Asp Trp Gln Met Leu Ala
                580                  585                  590
Gln Lys Asn Ser Ile Asn Arg Asn Leu Ser Tyr Phe Ala Thr Gln Ser
            595                  600                  605
Ser Pro Ser Ala Val Ile Leu Asn Leu Trp Glu Ala Arg His Gln His
        610                  615                  620
Asp Gly Asp Leu Asp Ser Leu Ala Cys Ala Leu Glu Glu Ile Gly Arg
625                  630                  635                  640
Thr His Thr Lys Leu Ser Asn Ile Ser Glu Ser Gln Leu Asp Glu Ala
                645                  650                  655
Asp Phe Asn Tyr Ser Arg Gln Asn Gly Leu
            660                  665
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<210> 31
<211> 1968
<212> DNA
<213> homo sapiens

<400> 31

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atggcagcca acatcgtggc taagaggaga agcctgtcgg ccactgttgt ggtctacgtg      60
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cggatccggg agtgcacagc accacccccg agaaatgggg gcaaattctg tgaaggtcta     180
agccaggaat ctgaaaactg cacagatggt ctttgcatcc taggcattga gaatgccagc     240
gacattgctt tgtactcggg cttgggtgct gccgtcgtgg ccgttgcagt cctggtcatt     300
ggtgtcaccc tttacagacg gagccagagt gactatggcg tggacgtcat tgactcttct     360
gcattgacag gtggcttcca gaccttcaac ttcaaaacag tccgtcaagg taactccctg     420
ctcctgaatt ctgccatgca gccagatctg acagtgagcc ggacatacag cggacccatc     480
tgtctgcagg accctctgga caaggagctc atgacagagt cctcactctt taccctttg      540
tcggacatca aagtgaaagt ccagagctcg ttcatggttt ccctgggagt gtctgagaga     600
gctgagtacc acggcaagaa tcattccagg acttttcccc atggaaacaa ccacagcttt     660
agtacaatgc atcccagaaa taaaatgccc tacatccaaa atctgtcatc actccccaca     720
aggacagaac tgaggacaac tggtgtcttt ggccatttag gggggcgctt agtaatgcca     780
aatacagggg tgagcttact cataccacac ggtgccatcc cagaggagaa ttcttgggag     840
atttatatgt ccatcaacca aggtgaaccc agcctccagt cagatggctc tgaggtgctc     900
ctgagtcctg aagtcacctg tggtcctcca gacatgatcg tcaccactcc ctttgcattg     960
accatcccgc actgtgcaga tgtcagttct gagcattgga atatccattt aaagaagagg    1020
acacagcagg gcaaatggga ggaagtgatg tcagtggaag atgaatctac atcctgttac    1080
tgccttttgg acccctttgc gtgtcatgtg ctcctggaca gctttgggac ctatgcgctc    1140
actggagagc caatcacaga ctgtgccgtg aagcaactga aggtggcggt ttttggctgc    1200
atgtcctgta actccctgga ttacaacttg agagtttact gtgtggacaa taccccttgt    1260
gcatttcagg aagtggtttc agatgaaagg catcaaggtg gacagctcct ggaagaacca    1320
aaattgctgc atttcaaagg gaataccttt agtcttcaga tttctgtcct tgatattccc    1380
ccattcctct ggagaattaa accattcact gcctgccagg aagtcccgtt ctcccgcgtg    1440
tggtgcagta accggcagcc cctgcactgt gccttctccc tggagcgtta tacgcccact    1500
accacccagc tgtcctgcaa aatctgcatt cggcagctca aaggccatga acagatcctc    1560
caagtgcaga catcaatcct agagagtgaa cgagaaacca tcactttctt cgcacaagag    1620
gacagcactt tccctgcaca gactggcccc aaagccttca aaattcccta ctccatcaga    1680
cagcggattt gtgctacatt tgataccccc aatgccaaag caaggactg gcagatgtta     1740
gcacagaaaa acagcatcaa caggaattta tcttatttcg ctacacaaag tagcccatct    1800
gctgtcattt tgaacctgtg ggaagctcgt catcagcatg atggtgatct tgactccctg    1860
gcctgtgccc ttgaagagat tgggaggaca cacacgaaac tctcaaacat ttcagaatcc    1920
cagcttgatg aagccgactt caactacagc aggcaaaatg gactctag              1968
```

<210> 32
<211> 655

34

<212> PRT
<213> homo sapiens

<400> 32
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Met Ala Ala Asn Ile Val Ala Lys Arg Arg Ser Leu Ser Ala Thr Val
 1               5                  10              15
Val Val Tyr Val Asp Gly Ser Trp Glu Val Trp Ser Glu Trp Ser Val
          20              25              30
Cys Ser Pro Glu Cys Glu His Leu Arg Ile Arg Glu Cys Thr Ala Pro
          35                  40                  45
Pro Pro Arg Asn Gly Gly Lys Phe Cys Glu Gly Leu Ser Gln Glu Ser
          50                  55                  60
Glu Asn Cys Thr Asp Gly Leu Cys Ile Leu Gly Ile Glu Asn Ala Ser
 65                  70                  75                  80
Asp Ile Ala Leu Tyr Ser Gly Leu Gly Ala Ala Val Val Ala Val Ala
                85                  90                  95
Val Leu Val Ile Gly Val Thr Leu Tyr Arg Arg Ser Gln Ser Asp Tyr
               100                 105                 110
Gly Val Asp Val Ile Asp Ser Ser Ala Leu Thr Gly Gly Phe Gln Thr
               115                 120                 125
Phe Asn Phe Lys Thr Val Arg Gln Gly Asn Ser Leu Leu Leu Asn Ser
      130                 135                 140
Ala Met Gln Pro Asp Leu Thr Val Ser Arg Thr Tyr Ser Gly Pro Ile
145                 150                 155                 160
Cys Leu Gln Asp Pro Leu Asp Lys Glu Leu Met Thr Glu Ser Ser Leu
               165                 170                 175
Phe Asn Pro Leu Ser Asp Ile Lys Val Lys Val Gln Ser Ser Phe Met
      180                 185                 190
Val Ser Leu Gly Val Ser Glu Arg Ala Glu Tyr His Gly Lys Asn His
          195                 200                 205
Ser Arg Thr Phe Pro His Gly Asn Asn His Ser Phe Ser Thr Met His
      210                 215                 220
Pro Arg Asn Lys Met Pro Tyr Ile Gln Asn Leu Ser Ser Leu Pro Thr
225                 230                 235                 240
Arg Thr Glu Leu Arg Thr Thr Gly Val Phe Gly His Leu Gly Gly Arg
               245                 250                 255
Leu Val Met Pro Asn Thr Gly Val Ser Leu Leu Ile Pro His Gly Ala
               260                 265                 270
Ile Pro Glu Glu Asn Ser Trp Glu Ile Tyr Met Ser Ile Asn Gln Gly
          275                 280                 285
Glu Pro Ser Leu Gln Ser Asp Gly Ser Glu Val Leu Leu Ser Pro Glu
      290                 295                 300
Val Thr Cys Gly Pro Pro Asp Met Ile Val Thr Thr Pro Phe Ala Leu
305                 310                 315                 320
Thr Ile Pro His Cys Ala Asp Val Ser Ser Glu His Trp Asn Ile His
               325                 330                 335
Leu Lys Lys Arg Thr Gln Gln Gly Lys Trp Glu Glu Val Met Ser Val
               340                 345                 350
Glu Asp Glu Ser Thr Ser Cys Tyr Cys Leu Leu Asp Pro Phe Ala Cys
               355                 360                 365
His Val Leu Leu Asp Ser Phe Gly Thr Tyr Ala Leu Thr Gly Glu Pro
      370                 375                 380
Ile Thr Asp Cys Ala Val Lys Gln Leu Lys Val Ala Val Phe Gly Cys
385                 390                 395                 400
Met Ser Cys Asn Ser Leu Asp Tyr Asn Leu Arg Val Tyr Cys Val Asp
               405                 410                 415
```

35

```
Asn Thr Pro Cys Ala Phe Gln Glu Val Val Ser Asp Glu Arg His Gln
          420                 425                 430
Gly Gly Gln Leu Leu Glu Glu Pro Lys Leu Leu His Phe Lys Gly Asn
          435                 440                 445
Thr Phe Ser Leu Gln Ile Ser Val Leu Asp Ile Pro Pro Phe Leu Trp
          450                 455                 460
Arg Ile Lys Pro Phe Thr Ala Cys Gln Glu Val Pro Phe Ser Arg Val
465                 470                 475                 480
Trp Cys Ser Asn Arg Gln Pro Leu His Cys Ala Phe Ser Leu Glu Arg
              485                 490                 495
Tyr Thr Pro Thr Thr Thr Gln Leu Ser Cys Lys Ile Cys Ile Arg Gln
          500                 505                 510
Leu Lys Gly His Glu Gln Ile Leu Gln Val Gln Thr Ser Ile Leu Glu
          515                 520                 525
Ser Glu Arg Glu Thr Ile Thr Phe Phe Ala Gln Glu Asp Ser Thr Phe
          530                 535                 540
Pro Ala Gln Thr Gly Pro Lys Ala Phe Lys Ile Pro Tyr Ser Ile Arg
545                 550                 555                 560
Gln Arg Ile Cys Ala Thr Phe Asp Thr Pro Asn Ala Lys Gly Lys Asp
              565                 570                 575
Trp Gln Met Leu Ala Gln Lys Asn Ser Ile Asn Arg Asn Leu Ser Tyr
          580                 585                 590
Phe Ala Thr Gln Ser Ser Pro Ser Ala Val Ile Leu Asn Leu Trp Glu
          595                 600                 605
Ala Arg His Gln His Asp Gly Asp Leu Asp Ser Leu Ala Cys Ala Leu
          610                 615                 620
Glu Glu Ile Gly Arg Thr His Thr Lys Leu Ser Asn Ile Ser Glu Ser
625                 630                 635                 640
Gln Leu Asp Glu Ala Asp Phe Asn Tyr Ser Arg Gln Asn Gly Leu
              645                 650                 655
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<210> 33
<211> 3411
<212> DNA
<213> homo sapiens

<400> 33
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agagcggcgg ccaccgcagg cggcggcgga ggggcgcgcc gctggctccc gtggctgggg     180
ctgtgcttct gggcggcagg gaccgcggct gccccgagga actgacaatg cgaagccctt     240
cccgaatcca tcccatcagc tcctgggaca ctgcctcatt tcatagagga gccagatgat     300
gcttatatta tcaagagcaa ccctattgca ctcaggtgca aagcgaggcc agccatgcag     360
atattcttca aatgcaacgg cgagtgggtc catcagaacg agcacgtctc tgaagagact     420
ctggacgaga gctcaggttt gaaggtccgc gaagtgttca tcaatgttac taggcaacag     480
gtggaggact ccatgggcc cgaggactat tggtgccagt gtgtggcgtg agccacctg     540
ggtacctcca agagcaggaa ggcctctgtg cgcatagcct atttacggaa aaactttgaa     600
caagacccac aaggaaggga agttcccatt gaaggcatga ttgtactgca ctgccgccca     660
ccagagggag tccctgctgc cgaggtggaa tggctgaaaa atgaagagcc cattgactct     720
gaacaagacg agaacattga caccagggct gaccataacc tgatcatcag gcaggcacgg     780
ctctcggact caggaaatta cacctgcatg gcagccaaca tcgtggctaa gaggagaagc     840
ctgtcggcca ctgttgtggt ctacgtggat gggagctggg aagtgtggag cgaatggtcc     900
gtctgcagtc cagagtgtga acatttgcgg atccgggagt gcacagcacc accccgaga     960
aatgggggca aattctgtga aggtctaagc caggaatctg aaaactgcac agatggtctt    1020
tgcatcctag ataaaaaacc tcttcatgaa ataaaacccc aaagcattga gaatgccagc    1080
gacattgctt tgtactcggg cttgggtgct gccgtcgtgg ccgttgcagt cctggtcatt    1140
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ggtgtcaccc tttacagacg gagccagagt gactatggcg tggacgtcat tgactcttct    1200
gcattgacag gtggcttcca gaccttcaac ttcaaaacag tccgtcaagc caagaatatc    1260
atggaactaa tgatacaaga aaaatccttt ggtaactccc tgctcctgaa ttctgccatg    1320
cagccagatc tgacagtgag ccggacatac agcggaccca tctgtctgca ggaccctctg    1380
gacaaggagc tcatgacaga gtcctcactc tttaacccct tgtcggacat caaagtgaaa    1440
gtccagagct cgttcatggt ttccctggga gtgtctgaga gagctgagta ccacggcaag    1500
aatcattcca ggactttttcc ccatggaaac aaccacagct ttagtacaat gcatcccaga    1560
aataaaatgc cctacatcca aaatctgtca tcactcccca caaggacaga actgaggaca    1620
actggtgtct ttggccattt aggggggcgc ttagtaatgc caaatacagg ggtgagctta    1680
ctcataccac acggtgccat cccagaggag aattcttggg agatttatat gtccatcaac    1740
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tgtggtcctc cagacatgat cgtcaccact ccctttgcat tgaccatccc gcactgtgca    1860
gatgtcagtt ctgagcattg gaatatccat ttaaagaaga ggacacagca gggcaaatgg    1920
gaggaagtga tgtcagtgga agatgaatct acatcctgtt actgcctttt ggaccccttt    1980
gcgtgtcatg tgctcctgga cagctttggg acctatgcgc tcactggaga gccaatcaca    2040
gactgtgccg tgaagcaact gaaggtggcg gttttttggct gcatgtcctg taactcccctg    2100
gattacaact tgagagttta ctgtgtggac aatacccctt gtgcatttca ggaagtggtt    2160
tcagatgaaa ggcatcaagg tggacagctc ctggaagaac caaaattgct gcatttcaaa    2220
gggaatacct ttagtcttca gatttctgtc cttgatattc ccccattcct ctggagaatt    2280
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ctagagagtg aacgagaaac catcactttc ttcgcacaag aggacagcac tttcccctgca    2520
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aacaggaatt tatcttattt cgctacacaa agtagcccat ctgctgtcat tttgaacctg    2700
tgggaagctc gtcatcagca tgatggtgat cttgactccc tggcctgtgc ccttgaagag    2760
attgggagga cacacgaa actctcaaac atttcagaat cccagcttga tgaagccgac    2820
ttcaactaca gcaggcaaaa tggactctag tccacttcct cccatgagac agagtgatgg    2880
ccagcttggg gacatttgct ttaaatggga aagaggccgc tttctgccca gtggcgttgg    2940
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ataggtaaaa catgttaata gggaagagta caagctctct tacatataag agggctctac    3060
tatctccttg gaatccacat ttgggttaac tcctcagatt tggagtggca aggataaaag    3120
tgagggcaga agtagctgtg ggaaaagatg agctatgata atgctgggaa ggcagagatt    3180
gattaagtgc atgctttgaa ataggttttt aatgatgtgc cccaaagggc cagctgattc    3240
tggtactaga ttgtcagagt tttctaccaa ctggcatctg tgatgtcaga gatcattgta    3300
aaaatggctt ttagacgtga aacaaggttg ccaacccatt tgtatgactt caacaacgtc    3360
aaggagggca tttagaattt agaatctgag cacatcacac cagcaccagc t              3411
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